

GP 1642

Docket No.: A7542.0000/P001-E  
(PATENT)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:  
Ginette Serrero

Application No.: Not Yet Assigned

Group Art Unit: 1642

Filed: April 4, 2001

Examiner: M. Wells

For: 88KDA TUMORIGENIC GROWTH  
FACTOR AND ANTAGONISTS

REQUEST TO USE COMPUTER READABLE FORM FROM ANOTHER  
APPLICATION

ATTN: Application Processing Division  
Assistant Commissioner for Patents  
Washington, DC 20231

Dear Sir:

The computer readable form in this divisional application, filed April 4, 2001, is identical with that filed in application numbers 08/991,862 filed on December 16, 1997 which is a continuation-in-part application of U.S. application serial number 08/863,079 filed on May 23, 1997. In accordance with 37 CFR 1.821(e), please use the only computer readable form filed in the applications as the computer readable form for the instant application. It is understood that the Patent and Trademark Office will make the necessary change in application number and filing date for the computer readable form that will be used for the instant application. A paper copy of the Sequence Listing is included in a separately filed preliminary amendment for incorporation into the specification.

Dated: April 4, 2001

Respectfully submitted,

By

~~James W. Brady, Jr.~~

~~Registration No.:~~ 32,115

Jeremy A. Cubert

Registration No.: 40,399

DICKSTEIN SHAPIRO MORIN &amp;

OSHINSKY LLP

2101 L Street NW

Washington, DC 20037-1526

(202) 775-4720

Attorneys for Applicant

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Atty. Docket No: Z9996.488/PQ01-A

In re patent application of

Serrero, Ginette

Serial No. 08/991,862

Filed: December 16, 1997

For: 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

STATEMENT TO SUPPORT FILING AND SUBMISSION IN  
ACCORDANCE WITH 37 C.F.R. §§ 1.821-1.825

Assistant Commissioner for Patents  
Washington, D.C. 20231  
**Box SEQUENCE**

Sir:

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

1. the submission, filed herewith in accordance with 37 C.F.R. § 1.821(g), does not include new matter;

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

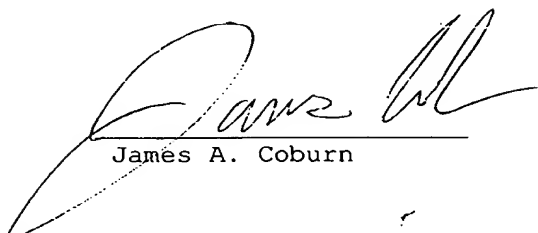
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. 08/991,

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

August 17, 1998  
Date

  
James A. Coburn

**HARBOR CONSULTING**  
Intellectual Property Services  
1500A Lafayette Road  
Suite 262  
Portsmouth, N.H.  
800-318-3021

# SEQUENCE LISTING

<110> Serrero, Ginette

<120> 88 KDA TUMORIGENIC GROWTH FACTOR AND ANTAGONISTS

<130> Z9996.488/P001-A

<140> 08/991,862

<141> 1997-12-16

<150> 08/863,862

<151> 1997-05-23

<160> 17

<170> PatentIn Ver. 2.0

<210> 1

<211> 2137

<212> DNA

<213> Mouse epithelin/granulin

<220>

<221> CDS

<222> (23)..(1789)

<223> The sequence is identical to that of the published mouse granulin except for one nucleotide (T instead of G) at position 1071 of GP88 cDNA (position 1056 of mouse granulin).

<400> 1

```

cggaccgccga cgcagacaga cc atg tgg gtc ctg atg agc tgg ctg gcc ttc 52
                        Met Trp Val Leu Met Ser Trp Leu Ala Phe
                          1                      5                      10

gcg gca ggg ctg gta gcc gga aca cag tgt cca gat ggg cag ttc tgc 100
Ala Ala Gly Leu Val Ala Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys
                        15                      20                      25

cct gtt gcc tgc tgc ctt gac cag gga gga gcc aac tac agc tgc tgt 148
Pro Val Ala Cys Cys Leu Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys
                        30                      35                      40

aac cct ctt ctg gac aca tgg cct aga ata acg agc cat cat cta gat 196
Asn Pro Leu Leu Asp Thr Trp Pro Arg Ile Thr Ser His His Leu Asp
                        45                      50                      55

ggc tcc tgc cag acc cat ggc cac tgt cct gct ggc tat tct tgt ctt 244
Gly Ser Cys Gln Thr His Gly His Cys Pro Ala Gly Tyr Ser Cys Leu
                        60                      65                      70

ctc act gtg tct ggg act tcc agc tgc tgc ccg ttc tct aag ggt gtg 292
Leu Thr Val Ser Gly Thr Ser Ser Cys Cys Pro Phe Ser Lys Gly Val
                        75                      80                      85

tct tgt ggt gat ggc tac cac tgc tgc ccc cag ggc ttc cac tgt agt 340
Ser Cys Gly Asp Gly Tyr His Cys Cys Pro Gln Gly Phe His Cys Ser
                        95                      100                      105

```

gca gat ggg aaa tcc tgc ttc cag atg tca gat aac ccc ttc ggt gct 388  
Ala Asp Gly Lys Ser Cys Phe Gln Met Ser Asp Asn Pro Leu Gly Ala  
110 115 120

gtc cag tgt cct ggg agc cag ttt gaa tgt cct gac tct gcc acc tgc 436  
Val Gln Cys Pro Gly Ser Gln Phe Glu Cys Pro Asp Ser Ala Thr Cys  
125 130 135

tgc att atg gtt gat ggt tgc tgg gga tgt tgt ccc atg ccc cag gcc 484  
Cys Ile Met Val Asp Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala  
140 145 150

tct tgc tgt gaa gac aga gtg cat tgc tgt ccc cat ggg gcc tcc tgt 532  
Ser Cys Cys Glu Asp Arg Val His Cys Cys Pro His Gly Ala Ser Cys  
155 160 165 170

gac ctg gtt cac aca cga tgc gtt tca ccc acg ggc acc cac acc cta 580  
Asp Leu Val His Thr Arg Cys Val Ser Pro Thr Gly Thr His Thr Leu  
175 180 185

cta aag aag ttc cct gca caa aag acc aac agc gca gtg tct ttg cct 628  
Leu Lys Lys Phe Pro Ala Gln Lys Thr Asn Ser Ala Val Ser Leu Pro  
190 195 200

ttt tct gtc gtg tgc cct gat gct aag acc cag tgt ccc gat gat tct 676  
Phe Ser Val Val Cys Pro Asp Ala Lys Thr Gln Cys Pro Asp Asp Ser  
205 210 215

acc tgc tgt gag cta ccc act ggg aag tat ggc tgc tgt cca atg ccc 724  
Thr Cys Cys Glu Leu Pro Thr Gly Lys Tyr Gly Cys Cys Pro Met Pro  
220 225 230

aat gcc atc tgc tgt tcc gac cac ctg cac tgc tgc ccc cag gac act 772  
Asn Ala Ile Cys Cys Ser Asp His Leu His Cys Cys Pro Gln Asp Thr  
235 240 245 250

gta tgt gac ctg atc cag agt aag tgc cta tcc aag aac tac acc acg 820  
Val Cys Asp Leu Ile Gln Ser Lys Cys Leu Ser Lys Asn Tyr Thr Thr  
255 260 265

gat ctc ctg acc aag ctg cct gga tac cca gtg aag gag gtg aag tgc 868  
Asp Leu Leu Thr Lys Leu Pro Gly Tyr Pro Val Lys Glu Val Lys Cys  
270 275 280

gac atg gag gtg agc tgc cct gaa gga tat acc tgc tgc cgc ctc aac 916  
Asp Met Glu Val Ser Cys Pro Glu Gly Tyr Thr Cys Cys Arg Leu Asn  
285 290 295

act ggg gcc tgg ggc tgc tgt cca ttt gcc aag gcc gtg tgt tgt gac 964  
Thr Gly Ala Trp Gly Cys Cys Pro Phe Ala Lys Ala Val Cys Cys Asp  
300 305 310

gat cac att cat tgc tgc ccg gca ggg ttt cag tgt cac aca gag aaa 1012  
Asp His Ile His Cys Cys Pro Ala Gly Phe Gln Cys His Thr Glu Lys  
315 320 325 330

gga acc tgc gaa atg ggt atc ctc caa gta ggg tgg atg aag aag gtc 1060  
Gly Thr Cys Glu Met Gly Ile Leu Gln Val Gly Trp Met Lys Lys Val  
335 340 345

ata gcc ccc ctc cgt cca gac cca cag atc ttg aag agt gat aca Ile Ala Pro Leu Arg Leu Pro Asp Pro Gln Ile Leu Lys Ser Asp Thr 350 355 360	1108
cct tgt gat gac ttc act agg tgt cct aca aac aat acc tgc tgc aaa Pro Cys Asp Asp Phe Thr Arg Cys Pro Thr Asn Asn Thr Cys Cys Lys 365 370 375	1156
ctc aat tct ggg gac tgg ggc tgc tgt ccc atc cca gag gct gtc tgc Leu Asn Ser Gly Asp Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys 380 385 390	1204
tgc tca gac aac cag cat tgc tgc cct cag ggc ttc aca tgt ctg gct Cys Ser Asp Asn Gln His Cys Cys Pro Gln Gly Phe Thr Cys Leu Ala 395 400 405 410	1252
cag ggg tac tgt cag aag gga gac aca atg gtg gct ggc ctg gag aag Gln Gly Tyr Cys Gln Lys Gly Asp Thr Met Val Ala Gly Leu Glu Lys 415 420 425	1300
ata cct gcc cgc cag aca acc ccg ctc caa att gga gat atc ggt tgt Ile Pro Ala Arg Gln Thr Thr Pro Leu Gln Ile Gly Asp Ile Gly Cys 430 435 440	1348
gac cag cat acc agc tgc cca gta ggg caa acc tgc tgc cca agc ctc Asp Gln His Thr Ser Cys Pro Val Gly Gln Thr Cys Cys Pro Ser Leu 445 450 455	1396
aag gga agt tgg gcc tgc tgc cag ctg ccc cat gct gtg tgc tgt gag Lys Gly Ser Trp Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu 460 465 470	1444
gac cgg cag cac tgt tgc ccg gcc ggg tac acc tgc aac gtg aag gcg Asp Arg Gln His Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala 475 480 485 490	1492
agg acc tgt gag aag gat gtc gat ttt atc cag cct ccc gtg ctc ctg Arg Thr Cys Glu Lys Asp Val Asp Phe Ile Gln Pro Pro Val Leu Leu 495 500 505	1540
acc ctc ggc cct aag gtt ggg aat gtg gag tgt gga gaa ggg cat ttc Thr Leu Gly Pro Lys Val Gly Asn Val Glu Cys Gly Glu Gly His Phe 510 515 520	1588
tgc cat gat aac cag acc tgt tgt aaa gac agt gca gga gtc tgg gcc Cys His Asp Asn Gln Thr Cys Cys Lys Asp Ser Ala Gly Val Trp Ala 525 530 535	1636
tgc tgt ccc tac cta aag ggt gtc tgc tgt aga gat gga cgt cac tgt Cys Cys Pro Tyr Leu Lys Gly Val Cys Cys Arg Asp Gly Arg His Cys 540 545 550	1684
tgc ccc ggt ggc ttc cac tgt tca gcc agg gga acc aag tgt ttg cga Cys Pro Gly Gly Phe His Cys Ser Ala Arg Gly Thr Lys Cys Leu Arg 555 560 565 570	1732
aag aag att cct cgc tgg gac atg ttt ttg agg gat ccg gtc cca aga Lys Lys Ile Pro Arg Trp Asp Met Phe Leu Arg Asp Pro Val Pro Arg 575 580 585	1780

ccg cta ctg taaggagg ctacagactt aaggaaactcc acagtcctg  
Pro Leu Leu

1829

gaaccctgtt ccgagggtac ccactactca ggccctcccta ggcctcctc ccctaacgtc 1889  
tccccggcct actcatcctg agtcacccta tcaccatggg aggtggagcc tcaaactaaa 1949  
accttctttt atggaaagaa ggctctggcc aaaagccccc tatcaaactg ccatttcttc 2009  
cggtttctgt ggaccttgtg gccaggtgct cttcccgagc cacaggtgtt ctgtgagctt 2069  
gcttgtgtgt gtgtgcgcgt gtgcgtgtgt tgctccaata aagtttgtac gctttctgaa 2129  
aaaaaaaa 2137

<210> 2

<211> 589

<212> PRT

<213> Mouse epithelin/granulin

<400> 2

Met Trp Val Leu Met Ser Trp Leu Ala Phe Ala Ala Gly Leu Val Ala  
1 5 10 15

Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu  
20 25 30

Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys Asn Pro Leu Leu Asp Thr  
35 40 45

Trp Pro Arg Ile Thr Ser His His Leu Asp Gly Ser Cys Gln Thr His  
50 55 60

Gly His Cys Pro Ala Gly Tyr Ser Cys Leu Leu Thr Val Ser Gly Thr  
65 70 75 80

Ser Ser Cys Cys Pro Phe Ser Lys Gly Val Ser Cys Gly Asp Gly Tyr  
85 90 95

His Cys Cys Pro Gln Gly Phe His Cys Ser Ala Asp Gly Lys Ser Cys  
100 105 110

Phe Gln Met Ser Asp Asn Pro Leu Gly Ala Val Gln Cys Pro Gly Ser  
115 120 125

Gln Phe Glu Cys Pro Asp Ser Ala Thr Cys Cys Ile Met Val Asp Gly  
130 135 140

Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp Arg  
145 150 155 160

Val His Cys Cys Pro His Gly Ala Ser Cys Asp Leu Val His Thr Arg  
165 170 175

Cys Val Ser Pro Thr Gly Thr His Thr Leu Leu Lys Lys Phe Pro Ala  
180 185 190

Gln Lys Thr Asn Ser Ala Val Ser Leu Pro Phe Ser Val Val Cys Pro  
195 200 205



Asp Ala Lys Thr Gln Cys Pro Asp Asp Ser Thr Cys Cys Glu Leu Pro  
210 215 220

Thr Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Ile Cys Cys Ser  
225 230 235 240

Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile Gln  
245 250 255

Ser Lys Cys Leu Ser Lys Asn Tyr Thr Thr Asp Leu Leu Thr Lys Leu  
260 265 270

Pro Gly Tyr Pro Val Lys Glu Val Lys Cys Asp Met Glu Val Ser Cys  
275 280 285

Pro Glu Gly Tyr Thr Cys Cys Arg Leu Asn Thr Gly Ala Trp Gly Cys  
290 295 300

Cys Pro Phe Ala Lys Ala Val Cys Cys Asp Asp His Ile His Cys Cys  
305 310 315 320

Pro Ala Gly Phe Gln Cys His Thr Glu Lys Gly Thr Cys Glu Met Gly  
325 330 335

Ile Leu Gln Val Gly Trp Met Lys Lys Val Ile Ala Pro Leu Arg Leu  
340 345 350

Pro Asp Pro Gln Ile Leu Lys Ser Asp Thr Pro Cys Asp Asp Phe Thr  
355 360 365

Arg Cys Pro Thr Asn Asn Thr Cys Cys Lys Leu Asn Ser Gly Asp Trp  
370 375 380

Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp Asn Gln His  
385 390 395 400

Cys Cys Pro Gln Gly Phe Thr Cys Leu Ala Gln Gly Tyr Cys Gln Lys  
405 410 415

Gly Asp Thr Met Val Ala Gly Leu Glu Lys Ile Pro Ala Arg Gln Thr  
420 425 430

Thr Pro Leu Gln Ile Gly Asp Ile Gly Cys Asp Gln His Thr Ser Cys  
435 440 445

Pro Val Gly Gln Thr Cys Cys Pro Ser Leu Lys Gly Ser Trp Ala Cys  
450 455 460

Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His Cys Cys  
465 470 475 480

Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Thr Cys Glu Lys Asp  
485 490 495

Val Asp Phe Ile Gln Pro Pro Val Leu Leu Thr Leu Gly Pro Lys Val  
500 505 510

Gly Asn Val Glu Cys Gly Glu Gly His Phe Cys His Asp Asn Gln Thr  
515 520 525

Cys Cys Lys Asp Ser Ala Gly Val Trp Ala Cys Cys Pro Tyr Leu Lys  
 530 535 540

Gly Val Cys Cys Arg Asp Gly Arg His Cys Cys Pro Gly Gly Phe His  
 545 550 555 560

Cys Ser Ala Arg Gly Thr Lys Cys Leu Arg Lys Lys Ile Pro Arg Trp  
 565 570 575

Asp Met Phe Leu Arg Asp Pro Val Pro Arg Pro Leu Leu  
 580 585

<210> 3  
 <211> 19  
 <212> PRT  
 <213> mouse granulin

<220>  
 <221> PEPTIDE  
 <222> (1)..(19)  
 <223> Internal peptide of mouse GP88 used to raise the  
 antisera against the GP88 used in the  
 immunoaffinity step.

<400> 3  
 Lys Lys Val Ile Ala Pro Arg Arg Leu Pro Asp Pro Gln Ile Leu Lys  
 1 5 10 15

Ser Asp Thr

<210> 4  
 <211> 12  
 <212> PRT  
 <213> mouse granulin

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> Internal peptide of mouse GP88 used to raise the  
 antisera against the GP88 used in the  
 immunoaffinity step.

<400> 4  
 Pro Asp Ala Lys Thr Gln Cys Pro Asp Asp Ser Thr  
 1 5 10

<210> 5  
 <211> 14  
 <212> PRT  
 <213> mouse granulin

<220>  
 <221> PEPTIDE  
 <222> (1)..(14)  
 <223> Internal peptide of mouse GP88 used to raise the  
 antisera against the GP88 used in the  
 immunoaffinity step.

<400> 5

Ser Ala Arg Gly Thr Lys Cys Leu Arg Lys Lys Ile Pro Arg  
1 5 10

<210> 6

<211> 19

<212> PRT

<213> Human granulin

<220>

<221> PEPTIDE

<222> (1)..(19)

<223> Internal peptide of human GP88 used to develop  
neutralizing anti-human GP88 monoclonal antibody.

<400> 6

Glu Lys Ala Pro Ala His Leu Ser Leu Pro Asp Pro Gln Ala Leu Lys  
1 5 10 15

Arg Asp Val

<210> 7

<211> 14

<212> PRT

<213> Human granulin

<220>

<221> PEPTIDE

<222> (1)..(14)

<223> Internal peptide of human GP88 used to develop  
neutralizing anti-human GP88 monoclonal antibody.

<400> 7

Ala Arg Arg Gly Thr Lys Cys Leu Arg Arg Glu Ala Pro Arg  
1 5 10

<210> 8

<211> 24

<212> DNA

<213> mammalian

<220>

<221> primer

<222> (1)..(24)

<223> Internal peptide of CMV promoter used as PCR  
primer.

<400> 8

cctacttggc agtacatcta cgta

24

<210> 9

<211> 27

<212> DNA

<213> mammalian

<220>  
<221> primer  
<222> (1)..(27)  
<223> GP88 cDNA start codon used as oligonucleotide PCR  
primer.

<400> 9  
cgagaattca ggcagaccat gtgggtc

27

<210> 10  
<211> 27  
<212> DNA  
<213> mammalian

<220>  
<221> primer  
<222> (1)..(27)  
<223> Antisense primer oligonucleotide primer

<400> 10  
cgagaattca ggcagaccat gtgggtc

27

<210> 11  
<211> 23  
<212> DNA  
<213> mammalian

<220>  
<221> primer  
<222> (1)..(23)  
<223> Antisense primer oligonucleotide primer

<400> 11  
ctgacgggtc actaaacgag etc

23

<210> 12  
<211> 25  
<212> DNA  
<213> mammalian

<220>  
<221> primer  
<222> (1)..(25)  
<223> primer

<400> 12  
ggatccacgg agttgttacc tgatc

25

<210> 13  
<211> 25  
<212> DNA  
<213> mammalian

<220>  
<221> primer  
<222> (1)..(25)  
<223> oligonucleotide PCR primer

<400> 13  
gaattcgag gcagaccatg tggac

25

<210> 14  
<211> 21  
<212> DNA  
<213> mammalian

<220>  
<221> primer  
<222> (1)..(21)  
<223> Antisense oligonucleotide to human GP88

<400> 14  
gggtccacat ggtctgcctg c

21

<210> 15  
<211> 24  
<212> DNA  
<213> mammalian

<220>  
<221> primer  
<222> (1)..(24)  
<223> Antisense oligonucleotide to human GP88

<400> 15  
gccaccagcc ctgctgttaa ggcc

24

<210> 16  
<211> 2095  
<212> DNA  
<213> Human GP88 cDNA

<220>  
<221> CDS  
<222> (13)..(1791)  
<223> Nucleotide sequence of human granulin/epithelin  
precursor (human GP88). Human Granulin Genebank  
M75161.

<400> 16  
cgcaggcaga cc atg tgg acc ctg gtg agc tgg gtg gcc tta aca gca ggg 51  
Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly  
1 5 10

ctg gtg gct gga acg cgg tgc cca gat ggt cag ttc tgc cct gtg gcc 99  
Leu Val Ala Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala  
15 20 25

tgc tgc ctg gac ccc gga gga gcc agc tac agc tgc tgc cgt ccc ctt 147  
Cys Cys Leu Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu  
30 35 40 45

ctg gac aaa tgg ccc aca aca ctg agc agg cat ctg ggt ggc ccc tgc 195  
Leu Asp Lys Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys  
50 55 60

cag gtt gat gcc cac tgc tct gcc ggc cac tcc tgc atc ttt acc gtc Gln Val Asp Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val	243
65 70 75	
tca ggg act tcc agt tgc tgc ccc ttc cca gag gcc gtg gca tgc ggg Ser Gly Thr Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly	291
80 85 90	
gat ggc cat cac tgc tgc cca cgg ggc ttc cac tgc agt gca gac ggg Asp Gly His His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly	339
95 100 105	
cga tcc tgc ttc caa aga tca ggt aac aac tcc gtg ggt gcc atc cag Arg Ser Cys Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln	387
110 115 120 125	
tgc cct gat agt cag ttc gaa tgc ccg gac ttc tcc acg tgc tgt gtt Cys Pro Asp Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val	435
130 135 140	
atg gtc gat ggc tcc tgg ggg tgc tgc ccc atg ccc cag gct tcc tgc Met Val Asp Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys	483
145 150 155	
tgt gaa gac agg gtg cac tgc tgt ccg cac ggt gcc ttc tgc gac ctg Cys Glu Asp Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu	531
160 165 170	
gtt cac acc cgc tgc atc aca ccc acg ggc acc cac ccc ctg gca aag Val His Thr Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys	579
175 180 185	
aag ctc cct gcc cag agg act aac agg gca gtg gcc ttg tcc agc tcg Lys Leu Pro Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Ser	627
190 195 200 205	
gtc atg tgt ccg gac gca cgg tcc cgg tgc cct gat ggt tct acc tgc Val Met Cys Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys	675
210 215 220	
tgt gag ctg ccc agt ggg aag tat ggc tgc tgc cca atg ccc aac gcc Cys Glu Leu Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala	723
225 230 235	
acc tgc tgc tcc gat cac ctg cac tgc tgc ccc caa gac act gtg tgt Thr Cys Cys Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys	771
240 245 250	
gac ctg atc cag agt aag tgc ctc tcc aag gag aac gct acc acg gac Asp Leu Ile Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp	819
255 260 265	
ctc ctc act aag ctg cct gcg cac aca gtg ggc gat gtg aaa tgt gac Leu Leu Thr Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp	867
270 275 280 285	
atg gag gtg agc tgc cca gat ggc tat acc tgc tgc cgt cta cag tcg Met Glu Val Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser	915
290 295 300	

ggg gcc tgg ggc tgc cct ttt acc cag gct gtg tgc cgt gac 963  
 Gly Ala Trp Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp  
 305 310 315

cac ata cac tgc tgt ccc gcg ggg ttt acg tgt gac acg cag aag ggt 1011  
 His Ile His Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly  
 320 325 330

acc tgt gaa cag ggg ccc cac cag gtg ccc tgg atg gag aag gcc cca 1059  
 Thr Cys Glu Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro  
 335 340 345

gct cac ctc agc ctg cca gac cca caa gcc ttg aag aga gat gtc ccc 1107  
 Ala His Leu Ser Leu Pro Asp Pro Gln Ala Leu Lys Arg Asp Val Pro  
 350 355 360 365

tgt gat aat gtc agc agc tgt ccc tcc tcc gat acc tgc tgc caa ctc 1155  
 Cys Asp Asn Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu  
 370 375 380

acg tct ggg gag tgg ggc tgc tgt cca atc cca gag gct gtc tgc tgc 1203  
 Thr Ser Gly Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys  
 385 390 395

tcg gac cac cag cac tgc tgc ccc cag cga tac acg tgt gta gct gag 1251  
 Ser Asp His Gln His Cys Cys Pro Gln Arg Tyr Thr Cys Val Ala Glu  
 400 405 410

ggg cag tgt cag cga gga agc gag atc gtg gct gga ctg gag aag atg 1299  
 Gly Gln Cys Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met  
 415 420 425

cct gcc cgc cgc ggt tcc tta tcc cac ccc aga gac atc ggc tgt gac 1347  
 Pro Ala Arg Arg Gly Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp  
 430 435 440 445

cag cac acc agc tgc ccg gtg ggc gga acc tgc tgc ccg agc cag ggt 1395  
 Gln His Thr Ser Cys Pro Val Gly Gly Thr Cys Cys Pro Ser Gln Gly  
 450 455 460

ggg agc tgg gcc tgc tgc cag ttg ccc cat gct gtg tgc tgc gag gat 1443  
 Gly Ser Trp Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp  
 465 470 475

cgc cag cac tgc tgc ccg gct ggc tac acc tgc aac gtg aag gct cga 1491  
 Arg Gln His Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg  
 480 485 490

tcc tgc gag aag gaa gtg gtc tct gcc cag cct gcc acc ttc ctg gcc 1539  
 Ser Cys Glu Lys Glu Val Val Ser Ala Gln Pro Ala Thr Phe Leu Ala  
 495 500 505

cgt agc cct cac gtg ggt gtg aag gac gtg gag tgt ggg gaa gga cac 1587  
 Arg Ser Pro His Val Gly Val Lys Asp Val Glu Cys Gly Glu Gly His  
 510 515 520 525

ttc tgc cat gat aac cag acc tgc tgc cga gac aac cga cag ggc tgg 1635  
 Phe Cys His Asp Asn Gln Thr Cys Cys Arg Asp Asn Arg Gln Gly Trp  
 530 535 540

gcc tgc tgt ccc tac gcc cag ggc gtc tgt tgt gct gat cgg cgc cac 1683  
 Ala Cys Cys Pro Tyr Ala Gln Gly Val Cys Cys Ala Asp Arg Arg His  
 545 550 555

tgc tgt cct gct ggc ttc cgc tgc gca cgc agg ggt acc aag tgt ttg 1731  
 Cys Cys Pro Ala Gly Phe Arg Cys Ala Arg Arg Gly Thr Lys Cys Leu  
 560 565 570

cgc agg gag gcc ccg cgc tgg gac gcc cct ttg agg gac cca gcc ttg 1779  
 Arg Arg Glu Ala Pro Arg Trp Asp Ala Pro Leu Arg Asp Pro Ala Leu  
 575 580 585

aga cag ctg ctg tgagggacag tactgaagac tctgcagccc tcgggacccc 1831  
 Arg Gln Leu Leu  
 590

actcggaggg tgccctctgc tcaggcctcc ctacacctc cccctaacca aattctccct 1891  
 ggaccccatt ctgagctccc catcaccatg ggaggtgggg cctcaatcta aggcccttcc 1951  
 ctgtcagag ggggttgagg caaaagccca ttacaagctg ccacccctc cccgtttcag 2011  
 tggaccctgt ggccaggtgc ttttcctat ccacaggggt gtttgtgtgt tgggtgtgct 2071  
 ttcaataaag tttgtcactt tctt 2095

<210> 17  
 <211> 593  
 <212> PRT  
 <213> Human GP88 cDNA

<400> 17  
 Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala  
 1 5 10 15  
 Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu  
 20 25 30  
 Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys  
 35 40 45  
 Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp  
 50 55 60  
 Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr  
 65 70 75 80  
 Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His  
 85 90 95  
 His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys  
 100 105 110  
 Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp  
 115 120 125  
 Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp  
 130 135 140



Gly Ser Trp Gly Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp  
 145 150 155 160

Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr  
 165 170 175

Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro  
 180 185 190

Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Ser Val Met Cys  
 195 200 205

Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu  
 210 215 220

Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys  
 225 230 235 240

Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile  
 245 250 255

Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr  
 260 265 270

Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val  
 275 280 285

Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp  
 290 295 300

Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His  
 305 310 315 320

Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu  
 325 330 335

Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu  
 340 345 350

Ser Leu Pro Asp Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn  
 355 360 365

Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly  
 370 375 380

Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His  
 385 390 395 400

Gln His Cys Cys Pro Gln Arg Tyr Thr Cys Val Ala Glu Gly Gln Cys  
 405 410 415

Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg  
 420 425 430

Arg Gly Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr  
 435 440 445

Ser Cys Pro Val Gly Gly Thr Cys Cys Pro Ser Gln Gly Gly Ser Trp  
 450 455 460

Ala Cys Cys Gln Leu His Ala Val Cys Cys Glu Asp Gln His  
 465 475 480  
 Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Ser Cys Glu  
 485 490 495  
 Lys Glu Val Val Ser Ala Gln Pro Ala Thr Phe Leu Ala Arg Ser Pro  
 500 505 510  
 His Val Gly Val Lys Asp Val Glu Cys Gly Glu Gly His Phe Cys His  
 515 520 525  
 Asp Asn Gln Thr Cys Cys Arg Asp Asn Arg Gln Gly Trp Ala Cys Cys  
 530 535 540  
 Pro Tyr Ala Gln Gly Val Cys Cys Ala Asp Arg Arg His Cys Cys Pro  
 545 550 555 560  
 Ala Gly Phe Arg Cys Ala Arg Arg Gly Thr Lys Cys Leu Arg Arg Glu  
 565 570 575  
 Ala Pro Arg Trp Asp Ala Pro Leu Arg Asp Pro Ala Leu Arg Gln Leu  
 580 585 590

Leu